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Reviewer Comments:
1.
<210>   17
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<212>   PRT
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<223>   Consensus peptide sequence
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<221>   X
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<223>   X = any amino acid with at least one cysteine residue having the
        formula (Xaa)n, where Xaa is any amino acid and n is an integer
        from 1 to 20
<220>
<221>   X
<222>   (2)..(2)
<223>   X = W or F
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<221>   X
<222>   (3)..(17)
<223>   X = any positively charged amino acid
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<221>   X
<222>   (18)..(18)
<223>   X = W or F
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<223>   X = any amino acid

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       formula (Xaa)n, where Xaa is any amino acid and n is an integer
       from 1 to 20
* * * * * * * *
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For SEQ ID # 17, 18,19,21,22, and 23, "Xaa" cannot represent more than one amino acid. For example, SEQ ID # 17 says the "Xaa" at positions 1 and 33 can represent 1 to 20 amino acids. Please make all necessary changes.

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2.
W213           Artificial or Unknown found in <213> in SEQ ID (1)
E257           Invalid sequence data feature in <221> in SEQ ID (1)
E257           Invalid sequence data feature in <221> in SEQ ID (1)
E257           Invalid sequence data feature in <221> in SEQ ID (1)
E257           Invalid sequence data feature in <221> in SEQ ID (1)
E257           Invalid sequence data feature in <221> in SEQ ID (1)
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W213           Artificial or Unknown found in <213> in SEQ ID (5)
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E257            Invalid sequence data feature in <221> in SEQ ID (17)
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W213            Artificial or Unknown found in <213> in SEQ ID (19)
E257            Invalid sequence data feature in <221> in SEQ ID (19)
E257            Invalid sequence data feature in <221> in SEQ ID (19)
This error has occured more than 20 times, will not be displayed
W213            Artificial or Unknown found in <213> in SEQ ID (20) This
error has occured more than 20 times, will not be displayed

The warnings and errors shown above are ok and require no response.
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Application No: 10551619   Version No: 3.0

Input Set:

Output Set:

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Finished:	2009-06-08 13:02:26.403
Elapsed:	0 hr(s) 0 min(s) 15 sec(s) 112 ms
Total Warnings:	33
Total Errors:	58
No. of SeqIDs Defined:	33
Actual SeqID Count:	33

Error code		Error Description
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E	257	Invalid sequence data feature in <221> in SEQ ID (1)
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E	257	Invalid sequence data feature in <221> in SEQ ID (1)
W	213	Artificial or Unknown found in <213> in SEQ ID (2)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
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W	213	Artificial or Unknown found in <213> in SEQ ID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
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W	213	Artificial or Unknown found in <213> in SEQ ID (14)
W	213	Artificial or Unknown found in <213> in SEQ ID (15)

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              Input Set:


              Output Set:



            Started:  2009-06-08 13:02:11.291
           Finished:  2009-06-08 13:02:26.403
            Elapsed:  0 hr(s) 0 min(s) 15 sec(s) 112 ms
     Total Warnings:  33
       Total Errors:  58
No. of SeqIDs Defined:  33
  Actual SeqID Count:  33
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Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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E 257	Invalid sequence data feature in <221> in SEQ ID (19) This error has occured more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occured more than 20 times, will not be displayed

                          SEQUENCE LISTING

<110>   The Regents of the University of California
        Martin, Paul Taylor

<120>   AMYLOID-SPECIFIC PEPTIDES AND USES THEREOF

<130>   00015-022US1

<140>   10551619
<141>   2006-12-22

<150>   US 60/461,168
<151>   2003-04-07

<150>   PCT/US04/10939
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<170>   PatentIn version 3.3

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Asp Trp Gly Lys Gly Gly Arg Trp Arg Leu Trp Pro Gly Ala Ser Gly
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Lys Thr Glu Ala
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Cys Asp Trp Gly Lys Gly Gly Arg Trp Arg Leu Trp Pro Gly Ala Ser
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Cys Pro Gly Arg Ser Pro Phe Thr Gly Lys Lys Leu Phe Asn Gln Glu
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Phe Ser Gln Asp Gln Cys
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<220>
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<210>   9
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Lys Gly Arg Arg
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<210>   11
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Gln Gly Gly Arg
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Arg Asn Leu Glu
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<210> 14
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<210>   16
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Leu Ile Arg Arg
            20

<210>   17
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       from 1 to 20

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<222> (2)..(2)
<223> X = W or F

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       from 1 to 20

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         20   25   30

Xaa

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      from 1 to 20

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        20   25   30

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      from 1 to 20

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            20   25   30

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30


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       from 1 to 20

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1               5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        20                  25                  30


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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1                   5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
         35                  40



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       from 1 to 20


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1                5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35                  40



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1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                    20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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<212>   PRT
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<223>   Phage display peptide library sequence

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<212>   PRT
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<212>  PRT
<213>  Artificial sequence

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Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
            20                  25                  30


Gly Leu Met Val Gly Gly Val Val
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gtttgtcgtc tttccagacg                                                   20


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<213>  Artificial sequence

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gtcggggaag acggaggcgt gcggcccgcc gtattagtct agagc                      105


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<213> Artificial sequence

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cgccaccgac ccccccttccc ccaatcgcat tctgcaggta ccccg   105

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<213> Artificial sequence

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<223> Flanking sequence from phage coat

<400> 32

Cys Gly Pro Pro Tyr
1   5

<210> 33
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus peptide sequence

<220>
<221> X
<222> (1)..(1)
<223> X = W or F

<220>
<221> X
<222> (2)..(6)
<223> X = any positively charged amino acid

<220>
<221> X
<222> (7)..(7)
<223> X = W or F

<220>
<221> X
<222> (8)..(10)
<223> X = any amino acid

<220>
<221> X
<222> (11)..(11)

<223> X = W or F

<400> 33

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10